

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/997,807B
Source: 1FW16
Date Processed by STIC: 3/30/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/30/2005

PATENT APPLICATION: US/09/997,807B

TIME: 15:21:33

Input Set : D:\56446-20109.00 - SEQ Substitute (client).txt

Output Set: N:\CRF4\03302005\I997807B.raw

4 <110> APPLICANT: Jay Short
 5 Eric Mathur
 6 William Michael Lafferty
 7 Nelson Barton
 8 Kevin Chow
 10 <120> TITLE OF INVENTION: Method of Making a Protein Polymer and Uses of the Polymer
 12 <130> FILE REFERENCE: 564462010900
 14 <140> CURRENT APPLICATION NUMBER: 09/997,807B
 15 <141> CURRENT FILING DATE: 2001-11-30
 17 <150> PRIOR APPLICATION NUMBER: 60/250,426
 18 <151> PRIOR FILING DATE: 2000-11-30
 20 <160> NUMBER OF SEQ ID NOS: 37
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 624
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Pyrodictium abyssi
 29 <400> SEQUENCE: 1.
 30 gtgaagtaca caaccctagc tatagcgggt attattgcct cggctgccgc cctcgccctc 60
 31 ctagcaggct tcgccaccac ccagagcccc ctcaacagct tctacgccac cgggtacagca 120
 32 caggcagtaa gcgagccaat agacgtagaa agccacctcg gcagcataac ccccgagcc 180
 33 ggcgcacagg gcagtgacga cataggttac gcaatagtgt ggataaagga ccaggtcaat 240
 34 gatgtaaagc tgaaggtgac cctgcgtaac gctgagcagc taaagcccta cttcaagtac 300
 35 ctacagatac agataacaag cggctatgag acgaacagca cagctctagg caacttcagc 360
 36 gagaccaagg ctgtgataag cctcgacaac cccagcgccg tgatagtact agacaaggag 420
 37 gatatagcag tgctctatcc ggacaagacc ggttacacaa acacttcgat atgggtaccc 480
 38 ggtgaacctg acaagataat tgtctacaac gagacaaagc cagtagctat actgaacttc 540
 39 aaggccttct acgaggctaa ggagggtatg ctattcgaca gcctgccagt gatattcaac 600
 40 ttccaggtgc tacaagtagg ctaa 624
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 207
 44 <212> TYPE: PRT
 45 <213> ORGANISM: Pyrodictium abyssi
 47 <400> SEQUENCE: 2
 48 Val Lys Tyr Thr Thr Leu Ala Ile Ala Gly Ile Ile Ala Ser Ala Ala
 49 1 5 10 15
 50 Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Asn
 51 20 25 30
 52 Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
 53 35 40 45
 54 Val Glu Ser His Leu Gly Ser Ile Thr Pro Ala Ala Gly Ala Gln Gly
 55 50 55 60
 56 Ser Asp Asp Ile Gly Tyr Ala Ile Val Trp Ile Lys Asp Gln Val Asn

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57 65          70          75          80
58 Asp Val Lys Leu Lys Val Thr Leu Arg Asn Ala Glu Gln Leu Lys Pro
59          85          90          95
60 Tyr Phe Lys Tyr Leu Gln Ile Gln Ile Thr Ser Gly Tyr Glu Thr Asn
61          100          105          110
62 Ser Thr Ala Leu Gly Asn Phe Ser Glu Thr Lys Ala Val Ile Ser Leu
63          115          120          125
64 Asp Asn Pro Ser Ala Val Ile Val Leu Asp Lys Glu Asp Ile Ala Val
65          130          135          140
66 Leu Tyr Pro Asp Lys Thr Gly Tyr Thr Asn Thr Ser Ile Trp Val Pro
67 145          150          155          160
68 Gly Glu Pro Asp Lys Ile Ile Val Tyr Asn Glu Thr Lys Pro Val Ala
69          165          170          175
70 Ile Leu Asn Phe Lys Ala Phe Tyr Glu Ala Lys Glu Gly Met Leu Phe
71          180          185          190
72 Asp Ser Leu Pro Val Ile Phe Asn Phe Gln Val Leu Gln Val Gly
73          195          200          205
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 513
77 <212> TYPE: DNA
78 <213> ORGANISM: Pyrodictium abyssi
80 <400> SEQUENCE: 3
81 gtgaagccta cggtcttagc cctggctggt atcattgcct cggtcgcca cctcgccctg      60
82 ctagcaggct tcgccaccac ccagagcccg ctcaacagct tctacgccac cggcacagca      120
83 gccgcaacaa gcgagccaat agacgtagag agccacctca gcagcatagc ccctgctgct      180
84 ggcgcacagg gcagccagga cataggctac ttcaacgtga ccgccaagga tcaagtgaac      240
85 gtgacaaaga taaaggtgac cctggctaac gctgagcagc taaagcccta cttcaagtac      300
86 ctacagatag tgctaaagag cgaggtagct gacgagatca aggccgtaat aagcatagac      360
87 aagcctagcg ccgtcataat actagacagc caggacttcg acagcaacaa cagagcaaag      420
88 ataagcgcca ctgcctacta cgaggctaag gagggcatgc tattcgacag cctaccgcta      480
89 atattcaaca tacaggtgct aagcgtcagc taa                                     513
91 <210> SEQ ID NO: 4
92 <211> LENGTH: 170
93 <212> TYPE: PRT
94 <213> ORGANISM: Pyrodictium abyssi
96 <400> SEQUENCE: 4
97 Val Lys Pro Thr Ala Leu Ala Leu Ala Gly Ile Ile Ala Ser Ala Ala
98 1          5          10          15
99 Asp Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Asn
100          20          25          30
101 Ser Phe Tyr Ala Thr Gly Thr Ala Ala Ala Thr Ser Glu Pro Ile Asp
102          35          40          45
103 Val Glu Ser His Leu Ser Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly
104          50          55          60
105 Ser Gln Asp Ile Gly Tyr Phe Asn Val Thr Ala Lys Asp Gln Val Asn
106 65          70          75          80
107 Val Thr Lys Ile Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys Pro
108          85          90          95
109 Tyr Phe Lys Tyr Leu Gln Ile Val Leu Lys Ser Glu Val Ala Asp Glu

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```

110          100          105          110
111 Ile Lys Ala Val Ile Ser Ile Asp Lys Pro Ser Ala Val Ile Ile Leu
112          115          120          125
113 Asp Ser Gln Asp Phe Asp Ser Asn Asn Arg Ala Lys Ile Ser Ala Thr
114          130          135          140
115 Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser Leu Pro Leu
116 145          150          155          160
117 Ile Phe Asn Ile Gln Val Leu Ser Val Ser
118          165          170
120 <210> SEQ ID NO: 5
121 <211> LENGTH: 537
122 <212> TYPE: DNA
123 <213> ORGANISM: Pyrodictium abyssi
125 <400> SEQUENCE: 5
126 atgaggtaca cgaccctagc tctggccggc atagtggcct cggctgccgc cctcgccctg      60
127 ctagcaggct tcgccacgac ccagagcccg ctaagcagct tctacgccac cggcacagca      120
128 caagcagtaa gcgagccaat agacgtagag agccacctag acaacaccat agcccctgct      180
129 gccggtgcac agggctacaa ggacatgggc tacattaaga taactaacca gtcaaaagtt      240
130 aatgtaataa agctgaaggt gactctcgct aacgccgagc agctaaagcc ctacttcgac      300
131 tacctacagc tagtactcac aagcaacgcc actggcaccg acatgggttaa ggctgtgcta      360
132 agcctcgaga agcctagcgc agtcataata ctagacaacg atgactacga tagcactaac      420
133 aagatacagc taaaggtaga agcctactat gaggctaagg agggcatgct attcgacagc      480
134 ctaccagtaa tactgaactt ccaggtactg agcgccgctt gcagtcctt gtggtga      537
136 <210> SEQ ID NO: 6
137 <211> LENGTH: 178
138 <212> TYPE: PRT
139 <213> ORGANISM: Pyrodictium abyssi
141 <400> SEQUENCE: 6
142 Met Arg Tyr Thr Thr Leu Ala Leu Ala Gly Ile Val Ala Ser Ala Ala
143 1          5          10          15
144 Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Ser
145          20          25          30
146 Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
147          35          40          45
148 Val Glu Ser His Leu Asp Asn Thr Ile Ala Pro Ala Ala Gly Ala Gln
149          50          55          60
150 Gly Tyr Lys Asp Met Gly Tyr Ile Lys Ile Thr Asn Gln Ser Lys Val
151 65          70          75          80
152 Asn Val Ile Lys Leu Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys
153          85          90          95
154 Pro Tyr Phe Asp Tyr Leu Gln Leu Val Leu Thr Ser Asn Ala Thr Gly
155          100          105          110
156 Thr Asp Met Val Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val
157          115          120          125
158 Ile Ile Leu Asp Asn Asp Asp Tyr Asp Ser Thr Asn Lys Ile Gln Leu
159          130          135          140
160 Lys Val Glu Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser
161 145          150          155          160
162 Leu Pro Val Ile Leu Asn Phe Gln Val Leu Ser Ala Ala Cys Ser Pro

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163                               165                               170                               175
164 Leu Trp
167 <210> SEQ ID NO: 7
168 <211> LENGTH: 395
169 <212> TYPE: DNA
170 <213> ORGANISM: Pyrodictium abyssi
172 <400> SEQUENCE: 7
173 agcttctacg ccaccggcac agcacaggca gtaagcgagc caatagacgt ggtaagcagc      60
174 ctcggtacgc taaatactgc cgctggtgca cagggttaagc agacgctagg agacataaca      120
175 atatatgcgc acaatgacgt gaacataaca aagctaaagg tcacgcttgc taacgctgca      180
176 cagctaagac catacttcaa gtacctgata ataaagctag taagcctgga cagcaacggc      240
177 aacgagtcgc agggaaaggg catgataact ctatggaagc cttacgccgt gataatacta      300
178 gaccatgaag atttcaacaa cgacatcgac aatgacggca acaatgacgc caagataagg      360
179 gttgtagcct actatgaggc taaggagggt atgct                                395
181 <210> SEQ ID NO: 8
182 <211> LENGTH: 131
183 <212> TYPE: PRT
184 <213> ORGANISM: Pyrodictium abyssi
186 <400> SEQUENCE: 8
187 Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
188 1           5           10          15
189 Val Val Ser Ser Leu Gly Thr Leu Asn Thr Ala Ala Gly Ala Gln Gly
190           20          25          30
191 Lys Gln Thr Leu Gly Asp Ile Thr Ile Tyr Ala His Asn Asp Val Asn
192           35          40          45
193 Ile Thr Lys Leu Lys Val Thr Leu Ala Asn Ala Ala Gln Leu Arg Pro
194           50          55          60
195 Tyr Phe Lys Tyr Leu Ile Ile Lys Leu Val Ser Leu Asp Ser Asn Gly
196 65          70          75          80
197 Asn Glu Ser Glu Glu Lys Gly Met Ile Thr Leu Trp Lys Pro Tyr Ala
198           85          90          95
199 Val Ile Ile Leu Asp His Glu Asp Phe Asn Asn Asp Ile Asp Asn Asp
200          100         105         110
201 Gly Asn Asn Asp Ala Lys Ile Arg Val Val Ala Tyr Tyr Glu Ala Lys
202          115         120         125
203 Glu Gly Met
204          130
206 <210> SEQ ID NO: 9
207 <211> LENGTH: 372
208 <212> TYPE: DNA
209 <213> ORGANISM: Pyrodictium abyssi
211 <400> SEQUENCE: 9
212 agcttctacg ccaccggcac agcagaggca acaagcgagc caatagacgt tgtaagcaac      60
213 cttaacacgg ccatagcccc tgctgccggc gccaggggca gcgtgggcat aggcagcata      120
214 acaatagaga acaagactga cgtgaacggt gtgaagctga agataaccct cgccaacgct      180
215 gagcagctaa agccctactt cgactacctt cagatagtgc taaagagcgt tgacagcaac      240
216 gagatcaagg ctgtgctaag cctcgagaag cccagcgagc tcataatact ggacaacgag      300
217 gacttcaggg gcggcgacaa ccagtgccag atagacgcc a ccgctacta cgaggctaag      360
218 gagggatatgc ta                                372

```

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220 <210> SEQ ID NO: 10
221 <211> LENGTH: 124
222 <212> TYPE: PRT
223 <213> ORGANISM: Pyrodictium abyssi
225 <400> SEQUENCE: 10
226 Ser Phe Tyr Ala Thr Gly Thr Ala Glu Ala Thr Ser Glu Pro Ile Asp
227 1 5 10 15
228 Val Val Ser Asn Leu Asn Thr Ala Ile Ala Pro Ala Ala Gly Ala Gln
229 20 25 30
230 Gly Ser Val Gly Ile Gly Ser Ile Thr Ile Glu Asn Lys Thr Asp Val
231 35 40 45
232 Asn Val Val Lys Leu Lys Ile Thr Leu Ala Asn Ala Glu Gln Leu Lys
233 50 55 60
234 Pro Tyr Phe Asp Tyr Leu Gln Ile Val Leu Lys Ser Val Asp Ser Asn
235 65 70 75 80
236 Glu Ile Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val Ile Ile
237 85 90 95
238 Leu Asp Asn Glu Asp Phe Gln Gly Gly Asp Asn Gln Cys Gln Ile Asp
239 100 105 110
240 Ala Thr Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu
241 115 120
243 <210> SEQ ID NO: 11
244 <211> LENGTH: 448
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: consensus sequence
251 <400> SEQUENCE: 11
252 tgagacccta gctgcggatt gcctcggtcg ccgcctcgcc ctctagcagg cttcgccaca 60
253 cccagagccc ctacagcttc tacgccaccg gcacagcaca ggcagtaagc gagccaatag 120
254 acgtagaaaag ccacctcaca catagcccct gctgccggcg cacagggcag caggacatag 180
255 gctacataaaa ataacaagat agtgaacgta taaagctgaa ggtgaccctg ctaacgctga 240
256 gcagctaaaag ccctacttca agtacctaca gatagtgcta aaagcgacag caggcacacg 300
257 agaaggcgtg ataagcctcg agaagcctag cgccgtcata atactagaca acgaggactt 360
258 cgaagcacaa cagaaagaga agcaatagcc tactacgagg ctaaggaggg tatgctattc 420
259 gacagcctcc tatataactc aggtctgt 448
261 <210> SEQ ID NO: 12
262 <211> LENGTH: 140
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: consensus sequence
269 <400> SEQUENCE: 12
270 Val Lys Thr Leu Ala Leu Ala Gly Ile Ile Ala Ser Ala Ala Leu Ala
271 1 5 10 15
272 Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Ser Phe Tyr Ala
273 20 25 30
274 Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp Val Glu Ser His
275 35 40 45

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/30/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 6,7,8,9,10

VERIFICATION SUMMARY

DATE: 03/30/2005

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Input Set : D:\56446-20109.00 - SEQ Substitute (client).txt

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L:375 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:379 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0